

OM protein - protein search, using sw model

Run on: December 13, 2004, 18:48:47 ; Search time 116.022 Seconds
(without alignments)
426.682 Million cell updates/sec

Title: US-10-010-942B-4 ,
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	718	99.9	138	5	ABG76924	Abg76924 Mouse 3D6
2	652	90.7	138	5	ABG76928	Abg76928 Humanised
3	651	90.5	468	6	ABP58275	Abp58275 Humanised
4	650	90.4	138	5	ABG76932	Abg76932 Humanised
5	609.5	84.8	133	6	ABG74243	Abg74243 Mouse ant
6	578.5	80.5	139	6	ABG74247	Abg74247 Mouse ant
7	578	80.4	462	6	AAO29869	Aao29869 Mouse ant
8	578	80.4	462	7	ADJ79787	Adj79787 TRA-8 ant
9	578	80.4	464	5	AAU72801	Aau72801 TRA-8 hea

10	573	79.7	138	2	AAR20064	Aar20064	MRK16-H c
11	569	79.1	144	5	ABB79730	Abb79730	Anti-Stre
12	568	79.0	139	2	AAR30480	Aar30480	hCEA spec
13	566	78.7	140	5	AAU76122	Aau76122	Mouse mon
14	564	78.4	139	2	AAR27053	Aar27053	Anti-CEA
15	564	78.4	140	5	AAU76133	Aau76133	Mouse mAb
16	563	78.3	138	2	AAW03722	Aaw03722	Anti-huma
17	561	78.0	140	5	AAU76132	Aau76132	Mouse mAb
18	560	77.9	138	3	AAV32404	Aay32404	Mouse ant
19	559	77.7	140	6	ABG74241	Abg74241	Mouse ant
20	557.5	77.5	137	2	AAW57592	Aaw57592	Chimeric
21	557.5	77.5	137	2	AAW89625	Aaw89625	Mouse hum
22	557.5	77.5	137	3	AAV77513	Aay77513	Mouse ant
23	557.5	77.5	137	4	AAG67102	Aag67102	Amino aci
24	557.5	77.5	137	4	AAG64775	Aag64775	Mouse ant
25	557.5	77.5	137	4	AAG63393	Aag63393	Amino aci
26	557.5	77.5	137	5	ABB95208	Abb95208	Mouse joi
27	557.5	77.5	137	6	ABJ36667	Abj36667	Angiogene
28	557.5	77.5	137	8	ADO33883	Ado33883	Murine pa
29	557	77.5	119	6	ABP58271	Abp58271	Humanised
30	557	77.5	449	6	ABP58273	Abp58273	Humanised
31	554.5	77.1	139	1	AAP90480	Aap90480	Chimeric
32	553	76.9	158	8	ADL27491	Adl27491	Amino aci
33	551	76.6	119	6	ABP58269	Abp58269	Humanised
34	551	76.6	158	2	AAW19579	Aaw19579	Mouse ant
35	551	76.6	477	2	AAR47450	Aar47450	T84.12 He
36	551	76.6	477	2	AAR47453	Aar47453	chiT84.12
37	550.5	76.6	141	8	ADO43551	Ado43551	Amino aci
38	549	76.4	140	2	AAW21841	Aaw21841	Heavy cha
39	549	76.4	247	2	AAW11917	Aaw11917	Murine MA
40	547.5	76.1	141	8	ADO43555	Ado43555	Amino aci
41	545	75.8	142	2	AAR30882	Aar30882	Antibody
42	542	75.4	140	7	ADC24966	Adc24966	Murine G2
43	542	75.4	140	7	ADK51721	Adk51721	Murine G2
44	539	75.0	136	2	AAR06251	Aar06251	Variable
45	539	75.0	138	3	AAV32406	Aay32406	Mouse ant

ALIGNMENTS

RESULT 1

ABG76924

ID ABG76924 standard; protein; 138 AA.

XX

AC ABG76924;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VH protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX
 OS Mus musculus...
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 DR N-PSDB; ABS59427.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Claim 68; Fig 2; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
 CC variable heavy (VH) chain protein of the invention
 XX
 SQ Sequence 138 AA;

Query Match 99.9%; Score 718; DB 5; Length 138;
 Best Local Similarity 99.3%; Pred. No. 7e-57;
 Matches 137; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

 Qy 121 YSGSSDYWGQGTITVTVSS 138
 |||||||||:||||
 Db 121 YSGSSDYWGQGTITVTVSS 138

RESULT 2
 ABG76928

ID ABG76928 standard; protein; 138 AA.
 XX
 AC ABG76928;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Humanised 3D6 heavy chain variable region #1.
 XX
 KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
 KW variable region complementarity determining region; 3D6; 10D5;
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
 KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
 KW Abeta.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Synthetic.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Claim 54; Page 155; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a humanized 3D6 variable light (VL) chain or variable
 CC heavy (VH) chain protein of the invention
 XX
 SQ Sequence 138 AA;

Query Match 90.7%; Score 652; DB 5; Length 138;
 Best Local Similarity 89.1%; Pred. No. 6.2e-51;
 Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||:|||||:| ||:|||||
 Db 1 MNFGLSLIFLVVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | |||:|||||:||||:|:|
 Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGT TVTVSS 138
 ||| |||
 Db 121 YSGSSDYWGQGT LVTVSS 138

RESULT 3

ABP58275

ID ABP58275 standard; protein; 468 AA.

XX

AC ABP58275;

XX

DT 23-OCT-2003 (revised)

DT 31-MAR-2003 (first entry)

XX

DE Humanised 3D6 antibody heavy chain.

XX

KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;

KW human; humanised antibody; antibody; Alzheimer's disease;

KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

XX

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .19
----	---------	--------

FT		/label= Signal_peptide
----	--	------------------------

FT	Protein	20. .468
----	---------	----------

FT		/label= Mature_peptide
----	--	------------------------

FT		/note= "the mature heavy chain is claimed in Claim 5"
----	--	---

FT	Region	20. .138
----	--------	----------

FT		/note= "heavy chain variable region, claimed in Claim 4"
----	--	--

FT	Region	50. .54
----	--------	---------

FT		/note= "CDR1"
----	--	---------------

FT	Region	69. .85
----	--------	---------

FT		/note= "CDR2"
----	--	---------------

FT	Region	118. .127
----	--------	-----------

FT		/note= "CDR3"
----	--	---------------

XX

PN WO200288306-A2.

XX

PD 07-NOV-2002.

XX

PF 26-APR-2002; 2002WO-US011853.

XX

PR 30-APR-2001; 2001US-0287539P.

XX

PA (ELIL) LILLY & CO ELI.

XX

QY 121 YSGSSDYWGQGTTVTVSS 138
 |||||
 Db 121 YSGSSDYWGQGTTLTVTVSS 138

RESULT 5

ABG74243

ID ABG74243 standard; protein; 133 AA.

XX

AC ABG74243;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3D8 heavy chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

KW small cell lung cancer; heavy chain variable region; mouse.

XX

OS Mus sp.

XX

PN US2002132983-A1.

XX

PD 19-SEP-2002.

XX

PF 10-DEC-2001; 2001US-00006773.

XX

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX

PA (JUNG/) JUNGHANS R P.

XX

PI Junghans RP;

XX

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16569.

XX

PT New chimeric molecule useful in treating patients with disorders, such as

PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer

PT comprises GD3 and/or PSMA binding domains of antibody.

XX

PS Disclosure; Page 12; 35pp; English.

XX

CC The invention relates to a chimaeric molecule comprising the GD3

CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)

CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

CC sequences, the zeta signalling chain of the T cell receptor and an

CC intervening CD8alpha hinge in which cysteine residues have been mutated.

CC The chimaeric molecules expressed in T cells or NK cells or other,

CC effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

CC and/or together with each other or with heterologous constructs to engage

CC additional stimulatory and functional properties of the effector cells to

KW Crohn's disease; diabetes mellitus; antibody; mouse.
 XX
 OS Mus sp.
 XX
 PN WO2003037913-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035333.
 XX
 PR 01-NOV-2001; 2001US-0346402P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
 XX
 DR WPI; 2003-441350/41.
 DR N-PSDB; AAL60477.
 XX
 PT New purified antibody that specifically binds a TNF-related apoptosis-
 PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
 PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
 PT rheumatoid arthritis.
 XX
 PS Example 16; Page 224-225; 251pp; English.
 XX
 CC The invention relates to an antibody that specifically binds a tumour
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 CC DR4 or DR5. Antibodies of the invention are useful for selectively
 CC inducing apoptosis in target cells expressing DR4, for inhibiting
 CC proliferation of target cells expressing DR4 or for treating cancer,
 CC inflammatory disease or autoimmune disease in a subject e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
 CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
 CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
 CC glomerular nephritis. The present sequence is mouse anti-human DR5
 CC antibody (TRA-8) heavy chain
 XX
 SQ Sequence 462 AA;

Query Match 80.4%; Score 578; DB 6; Length 462;
 Best Local Similarity 81.2%; Pred. No. 1.1e-43;
 Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||
 Db 1 MNFGLSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 :|||
 Db 61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSSLRSEDTAMYYCARRGD 120
 Qy 121 YSGSSDYWGQGTTVTVSS 138
 ::|||
 Db 121 SMITTDYWGQGTTLTVSS 138

RESULT 8

ADJ79787 .

ID ADJ79787 standard; protein; 462 AA.

XX

AC ADJ79787;

XX

DT 06-MAY-2004 (first entry)

XX

DE TRA-8 antibody heavy chain.

XX

KW nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;

KW antiallergic; antiinflammatory; antidiabetic; haemostatic;

KW neuroprotective; antiinfertility; immunosuppressive; dermatological;

KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;

KW proliferation;

KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;

KW TRAIL; synovial cell; lymphocyte; neutrophil;

KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;

KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;

KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;

KW autoimmune hemolytic anemia; sterility; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;

KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;

KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; hypoplastic anemia.

XX

OS Homo sapiens.

XX

PN WO2003038043-A2.

XX

PD 08-MAY-2003.

XX

PF 25-OCT-2002; 2002WO-US034420.

XX

PR 01-NOV-2001; 2001US-0346402P.

PR 24-JUN-2002; 2002US-0391478P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;

PI Lobuglio AF, Buchsbaum DJ;

XX

DR WPI; 2003-421518/39.

XX

PT Inducing apoptosis and inhibiting proliferation of target cells

PT expressing DR5, by contacting the target cell with an antibody that binds

PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic

PT agents.

XX

PS Example 16; SEQ ID NO 23; 274pp; English.

XX

CC The invention relates to a method of selectively inducing apoptosis in

CC and inhibiting (M1) proliferation of target cells expressing DR5,

CC comprising contacting the cell with an antibody that specifically binds

CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)

CC receptor DR5, where the antibody, in its soluble form, has in vivo and in

CC vitro apoptosis-inducing activity in the cell expressing DR5, and

contacting the cell with one or more therapeutic agents. M1 is useful for inducing apoptosis in target cell and inhibiting proliferation of target cell expressing DR5, where the target cell is an abnormally proliferating synovial cells (e.g. rheumatoid arthritis synovial cell), activated immune cell (e.g. activated lymphocyte), neutrophil, or virally infected cell. M2 is useful for treating a subject having inflammatory and autoimmune diseases. The inflammatory or autoimmune disease are selected from systemic lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia, thrombopenia, purpura, insulin dependent diabetes mellitus, allergy, asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, and hypoplastic anemia. This sequence represents a protein used in the method of the invention.

Sequence 462 AA;

Query Match 80.4%; Score 578; DB 7; Length 462;
Best Local Similarity 81.2%; Pred. No. 1.1e-43;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | : | | | | |

Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 YSGSSDYWGQGTTVTVSS 138
::|||||:||||

RESULT 9

ID AAU72801 standard; protein; 464 AA.

AC AAU72801;

XX
DT 26-FEB-2002 (first entry)

DE TRA-8 heavy chain.

KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.

OS Mus musculus.

XX

PN WO200183560-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014151.
 XX
 PR 02-MAY-2000; 2000US-0201344P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
 XX
 DR WPI; 2002-049338/06.
 DR N-PSDB; AAS97062.
 XX
 PT Novel antibody specific for tumor necrosis factor-related apoptosis-
 PT inducing ligand, useful for inhibiting cell proliferation in cancer.
 XX
 PS Claim 26; Page 198-199; 229pp; English.
 XX
 CC The invention describes a novel antibody which recognizes a tumour
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
 CC activity to a cell expressing DR5 in vivo. It is also useful for
 CC preparing a therapeutic for selective apoptosis of abnormal or
 CC dysregulated cells, and for inhibiting cell proliferation in a cell,
 CC preferably a human breast, ovary, colon, haematopoietic, prostate,
 CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
 CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
 CC antibody is used to treat an autoimmune disease, systemic lupus
 CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
 CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
 CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
 CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
 CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
 CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
 CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
 CC breast tissue. Peptides used to design primers for isolating heavy and
 CC light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
 CC shown in AAU72799 and AAU72800
 XX
 SQ Sequence 464 AA;

Query Match 80.4%; Score 578; DB 5; Length 464;
 Best Local Similarity 81.2%; Pred. No. 1.1e-43;
 Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||||||||||||||||| ||||||||||| |||||||||||:| |||||
 Db 1 MNFGLSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 :||||||:| ||| ||| |:|||||||:|||||||||:||||:| |
 Db 61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSSLRSEDTAMYVCARRGD 120

 Qy 121 YSGSSDYWGQGTTVTVSS 138

Db ::|||||||:||||
121 SMITTDYWGQGTTTLTVSS 138

RESULT 10

AAR20064

ID AAR20064 standard; protein; 138 AA.
XX
AC AAR20064;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1992 (first entry)
XX
DE MRK16-H chain.
XX
KW Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
XX
OS Homo; sapiens.
OS Mus musculus.
OS Chimeric.
XX
PN JP03254691-A.
XX
PD 13-NOV-1991.
XX
PF 02-MAR-1990; 90JP-00051563.
XX
PR 02-MAR-1990; 90JP-00051563.
XX
PA (GANK-) ZH GAN KENKYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX
DR WPI; 1992-002461/01.
DR N-PSDB; AAQ20070.
XX
PT Chimera antibody against drug resistant cancer - comprises variable
PT region homologous to region in mouse monoclonal antibody and constant
PT region homologous to region in human immunoglobulin.
XX
PS Disclosure; Fig 4; 20pp; Japanese.
XX
CC A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MRK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 138 AA;

Query Match

79.7%; Score 573; DB 2; Length 138;

Best Local Similarity 80.4%; Pred. No. 8.1e-44;

Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:||||| ||||| |||||:| |||||
Db      1 MNFGLSLIFLVLILKGVQCEVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          :|||||:| |||| ||| |:|||||:|||| |||||:||||| ||
Db     61 EKRLEWVATISSGGGNTYYPSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
          | |||| |||:
Db    121 YEAWFASWGQGTTLTVSA 138
```

RESULT 11

ABB79730

ID ABB79730 standard; protein; 144 AA.

XX

AC ABB79730;

XX

DT 29-OCT-2002 (first entry)

XX

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.

XX

KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy.

XX

OS Mus musculus.

XX

PN US2002068066-A1.

XX

PD 06-JUN-2002.

XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

DR WPI; 2002-565838/60.

DR N-PSDB; ABN84611.

XX

PT Treatment and prevention of dental caries in mammals, in particular
PT humans by orally administering genetically engineered or purified
PT antibodies that bind to surface antigens of carcinogenic organisms.

XX

PS Claim 14; Fig 3B; 30pp; English.

XX

CC The present sequence is the protein sequence of the heavy chain variable
CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFÉ was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion

XX

SQ Sequence 144 AA;

Query Match 79.1%; Score 569; DB 5; Length 144;
Best Local Similarity 78.2%; Pred. No. 2e-43;
Matches 111; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:|||||:|||| ||||||:||||| || ||||||:| |||||
Db 1 MDFGLSLVFLVLTCLKGVQCDVKLVESGGGLVNPGLSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVR--- 117
:||||||| ||| ||| |:|||||:|||||:|||||:||| |
Db 61 EKRLEWVASISSGGTYTYYPDSVKGRFTISRDNKNTLYLQMTSLKSEDTAMYYCSRDDG 120

Qy 118 -YDHYSGSSDYWGQGT TTVTVSS 138
| | : |||||:|||||
Db 121 SYGSYYYAMDYWGQGT SVTVSS 142

RESULT 12

AAR30480

ID AAR30480 standard; protein; 139 AA.

XX

AC AAR30480;

XX

DT 06-MAY-1993 (first entry)

XX

DE hCEA specific mouse heavy chain variable chain region.

XX

KW Chimeric antibody; human cancer embryonal antigen; treatment; diagnosis;
KW cancer.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /note= "signal peptide"

FT Protein 20. .139

FT /note= "mature peptide"

XX

PN JP04330295-A.

XX

PD 18-NOV-1992.

XX
 PF 28-DEC-1990; 90JP-00408811.
 XX
 PR 28-DEC-1990; 90JP-00408811.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 DR WPI; 1993-003502/01.
 DR N-PSDB; AAQ33052.
 XX
 PT Mouse-human chimeric antibody for diagnosis and treatment of cancer -
 PT obtd. by combining variable region of mouse antibody specifically
 PT combining to human cancer embryonic antigen with constant region of human
 PT antibody.
 XX
 PS Disclosure; Page 6; 10pp; Japanese.
 XX
 CC The sequence is that of the heavy chain variable region of a mouse
 CC antibody specific to human cancer embryonal antigen (hCEA). The region is
 CC used, with the corresponding mouse light chain variable region and the
 CC constant region of a human antibody, to prepare a mouse-human chimeric
 CC antibody which can be used for the diagnosis and treatment of cancer
 XX
 SQ Sequence 139 AA;

Query Match 79.0%; Score 568; DB 2; Length 139;
 Best Local Similarity 80.6%; Pred. No. 2.3e-43;
 Matches 112; Conservative 10; Mismatches 15; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||| |||||||||||||||||||||||||||||||||||||:| |||||
 Db 1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGSLKLSCAASGFTFSSYAMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 :||||||| | | ||| |:|||||||:||||| |||||||:|||||:| | :
 Db 61 EKRLEWVASITSDGS-TYYPDSVKGRFTISRDNARNILYLQMSSLRSED TAMYYCARVHY 119
 Qy 121 Y-SGSSDYWGQGTTVTVSS 138
 | | : |||||||:|||||
 Db 120 YDSPAMDYWGQGTSTVTVSS 138

RESULT 13

AAU76122

ID AAU76122 standard; protein; 140 AA.

XX

AC AAU76122;

XX

DT 08-MAY-2002 (first entry)

XX

DE Mouse monoclonal antibody 26-2F heavy chain variable region.

XX

KW Mouse; monoclonal antibody; heavy chain variable region; VH; angiogenin;

KW 26-2F; angiogenesis; tumour; cancer; retinopathy;

KW ocular neovascular disease; vitamin A deficiency; syphilis;

KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;

KW sickle cell anaemia; Paget's disease; mycobacterial infection;

KW osteoarthritis; graft versus host disease; autoimmune disease;
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .19
 FT /label= Signal_peptide
 FT Protein 20. .140
 FT /label= Mature_VH
 FT Region 50. .54
 FT /label= Complementarity_determining_region
 FT /note= "This region is specifically claimed in claim 3"
 FT Region 69. .85
 FT /label= Complementarity_determining_region
 FT /note= "This region is specifically claimed in claim 3"
 FT Region 118. .129
 FT /label= Complementarity_determining_region
 FT /note= "This region is specifically claimed in claim 3"
 XX
 PN US2002010320-A1.
 XX
 PD 24-JAN-2002.
 XX
 PF 05-APR-1999; 99US-00286240.
 XX
 PR 05-APR-1999; 99US-00286240.
 XX
 PA (FETT/) FETT J W.
 XX
 PI Fett JW;
 XX
 DR WPI; 2002-187790/24.
 DR N-PSDB; ABK15270.
 XX
 PT New antibody immunologically reactive to angiogenin useful for inhibiting
 PT angiogenesis and for treating conditions associated with abnormal
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
 PT arthritis.
 XX
 PS Claim 6; Page 14; 20pp; English.
 XX
 CC The invention relates to an antibody immunologically reactive to
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain
 CC nonhuman-derived complementarity determining regions having a binding
 CC affinity to the angiogenin or its fragment in combination with human
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
 CC included are an expression vector comprising a nucleic acid encoding the
 CC antibody and a host cell transformed with the vector. The antibody or its
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
 CC The antibody is useful for treating a tumour in humans, by inhibiting,
 CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
 CC ability of circulating tumour cell to form a vascularised tumour mass.
 CC The antibody is useful for treating a mammal with abnormal or unwanted
 CC angiogenesis, including cancer, and other diseases mediated by
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,

CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
 CC and retrolental fibroplasia, and other diseases associated with corneal
 CC neovascularisation including epidemic keratoconjunctivitis, vitamin A
 CC deficiency, contact lens overwear, atopic keratitis, superior limbic
 CC keratitis, syphilis, mycobacteria infections, lipid degeneration,
 CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
 CC infections, herpes zoster infections, protozoan infections, Kaposi's
 CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
 CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal
 CC graft rejection. Diseases associated with retinal/choroidal
 CC neovascularisation include macular degeneration, sickle cell anaemia,
 CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,
 CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
 CC disease, transplant rejection, autoimmune diseases such as type I
 CC diabetes, multiple sclerosis, systemic lupus erythematosus, and
 CC myasthenia gravis. The present sequence is the heavy chain variable
 CC region of mouse monoclonal antibody 26-2F

XX

SQ Sequence 140 AA;

Query Match 78.7%; Score 566; DB 5; Length 140;
 Best Local Similarity 79.3%; Pred. No. 3.5e-43;
 Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | : | | | : | | | : | | | | | | | | | | | | | | | | | | : | | | | |
 Db 1 MDFGLSWVFLVLILKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY-D 119
 : | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 61 EKRLEWVATISSGGGNTYYPDVKGRFTISRDIKNTLYLQMSSLRSEDTALYYCTRLGD 120

Qy 120 H-YSGSSDYWGQGT TVTVSS 138
 : | : : | | | | | : | | | | |
 Db 121 YGYAYTMDYWGQGT SVTVSS 140

RESULT 14

AAR27053

ID AAR27053 standard; protein; 139 AA.

XX

AC AAR27053;

XX

DT 01-MAR-1993 (first entry)

XX

DE Anti-CEA specific heavy chain variable region.

XX

KW Human; carcinoembryonic antigen; heavy chain; light chain; variable;
 KW region; diagnostic; tumour; markers; targetting.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /note= "signal peptide"

FT Protein 20. .139

FT /note= "mature peptide"

XX
 PN JP04234987-A.
 XX
 PD 24-AUG-1992.
 XX
 PF 28-DEC-1990; 90JP-00408810.
 XX
 PR 28-DEC-1990; 90JP-00408810.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 DR WPI; 1992-327631/40.
 DR N-PSDB; AAQ28746.
 XX
 PT New DNA fragments encoding variable regions of ABS specific for human CEA
 PT - for diagnosing and monitoring tumours, as tumour markers and for
 PT treatment of tumours.
 XX
 PS Disclosure; Fig 1; 7pp; Japanese.
 XX
 CC The anti-CEA murine monoclonal antibody heavy chain variable region was
 CC obtd. by screening a cDNA library prepd. from mRNA obtd. from hybridomas
 CC producing anti-CEA-specific antibodies with a probe based on the constant
 CC region of the H-chain. The antibodies reacts specifically with human CEA
 CC and are useful as a diagnostic agents, as tumour markers for digestive
 CC organs, for diagnosis of malignant tumours; for monitering after cancer
 CC operations, to follow up bloodless therapy or as therapeutic agents in
 CC passive immune therapy and targetting therapy. See also AAR27054
 XX
 SQ Sequence 139 AA;

Query Match 78.4%; Score 564; DB 2; Length 139;
 Best Local Similarity 79.9%; Pred. No. 5.3e-43;
 Matches 111; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||| -|||||
 Db 1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 :||||||| | | ||| |:|||||||:|:| |||||:|:|:| | :
 Db 61 EKRLEWVASITSDGS-TYYPDSVKGRFTISRDNARNILYLQMSSLRSEETAMYYCARVHY 119
 Qy 121 Y-SGSSDYWGQGTTVTVSS 138
 | | : |||||:||||
 Db 120 YDSPAMDYWGQGTSTVTVSS 138

RESULT 15

AAU76133

ID AAU76133 standard; protein; 140 AA.

XX

AC AAU76133;

XX

DT 08-MAY-2002 (first entry)

XX

DE Mouse mAb 26-2F heavy chain variable region mutant E59Y.

XX
 KW Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy;
 KW ocular neovascular disease; vitamin A deficiency; syphilis;
 KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;
 KW sickle cell anaemia; Paget's disease; mycobacterial infection;
 KW osteoarthritis; graft versus host disease; autoimmune disease;
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis; mutant; mutein; monoclonal antibody; 26-2F;
 KW heavy chain variable region; E59Y.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .19
 FT /label= Signal_peptide
 FT Protein 20. .140
 FT /label= Mature_VH
 FT Misc-difference 59
 FT /note= "Wild-type Glu substituted by Tyr"
 XX
 PN US2002010320-A1.
 XX
 PD 24-JAN-2002.
 XX
 PF 05-APR-1999; 99US-00286240.
 XX
 PR 05-APR-1999; 99US-00286240.
 XX
 PA (FETT/) FETT J W.
 XX
 PI Fett JW;
 XX
 DR WPI; 2002-187790/24.
 XX
 PT New antibody immunologically reactive to angiogenin useful for inhibiting
 PT angiogenesis and for treating conditions associated with abnormal
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
 PT arthritis.
 XX
 PS Claim 11; Page; 20pp; English.
 XX
 CC The invention relates to an antibody immunologically reactive to
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain
 CC nonhuman-derived complementarity determining regions having a binding
 CC affinity to the angiogenin or its fragment in combination with human
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
 CC included are an expression vector comprising a nucleic acid encoding the
 CC antibody and a host cell transformed with the vector. The antibody or its
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
 CC The antibody is useful for treating a tumour in humans, by inhibiting,
 CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
 CC ability of circulating tumour cell to form a vascularised tumour mass.
 CC The antibody is useful for treating a mammal with abnormal or unwanted
 CC angiogenesis, including cancer, and other diseases mediated by
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,
 CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:05:17 ; Search time 28.6222 Seconds
(without alignments)
319.748 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	566.5	78.8	135	3	US-08-579-378A-16	Sequence 16, Appl
2	563	78.3	138	2	US-08-379-057-14	Sequence 14, Appl
3	551	76.6	158	2	US-08-653-402B-6	Sequence 6, Appli
4	549	76.4	140	3	US-08-836-561-23	Sequence 23, Appl
5	549	76.4	140	4	US-09-434-122-23	Sequence 23, Appl
6	549	76.4	247	5	PCT-US94-07659-2	Sequence 2, Appli
7	545.5	75.9	135	3	US-08-579-378A-20	Sequence 20, Appl
8	541	75.2	136	3	US-08-976-183A-33	Sequence 33, Appl
9	540	75.1	136	3	US-08-976-183A-31	Sequence 31, Appl
10	537	74.7	136	3	US-08-976-183A-32	Sequence 32, Appl
11	536	74.5	136	3	US-08-976-183A-34	Sequence 34, Appl

12	535	74.4	136	1	US-08-253-877C-57	Sequence 57, Appl
13	535	74.4	136	2	US-08-452-164A-57	Sequence 57, Appl
14	535	74.4	138	1	US-08-053-171-7	Sequence 7, Appli
15	535	74.4	138	1	US-08-053-171-11	Sequence 11, Appl
16	535	74.4	158	2	US-08-653-402B-10	Sequence 10, Appl
17	514.5	71.6	139	1	US-08-129-930B-96	Sequence 96, Appl
18	514.5	71.6	139	3	US-08-134-346A-51	Sequence 51, Appl
19	514.5	71.6	139	3	US-08-976-288A-96	Sequence 96, Appl
20	513	71.3	170	2	US-08-652-558-40	Sequence 40, Appl
21	512.5	71.3	159	2	US-08-653-402B-2	Sequence 2, Appli
22	497.5	69.2	255	2	US-07-690-192-4	Sequence 4, Appli
23	494.5	68.8	463	4	US-09-472-087-1	Sequence 1, Appli
24	494.5	68.8	463	4	US-09-472-087-63	Sequence 63, Appl
25	494.5	68.8	463	4	US-09-472-087-64	Sequence 64, Appl
26	493	68.6	464	4	US-09-472-087-2	Sequence 2, Appli
27	493	68.6	464	4	US-09-472-087-66	Sequence 66, Appl
28	490.5	68.2	135	5	PCT-US95-07302-8	Sequence 8, Appli
29	486	67.6	130	4	US-09-225-322B-8	Sequence 8, Appli
30	486	67.6	130	4	US-09-764-304-8	Sequence 8, Appli
31	484.5	67.4	122	1	US-07-634-278-48	Sequence 48, Appl
32	484.5	67.4	122	1	US-08-477-728-48	Sequence 48, Appl
33	484.5	67.4	122	1	US-08-474-040-48	Sequence 48, Appl
34	484.5	67.4	122	1	US-08-487-200-48	Sequence 48, Appl
35	484.5	67.4	122	3	US-08-484-537-48	Sequence 48, Appl
36	484	67.3	130	4	US-09-225-322B-18	Sequence 18, Appl
37	484	67.3	130	4	US-09-764-304-18	Sequence 18, Appl
38	482.5	67.1	135	3	US-08-619-491-8	Sequence 8, Appli
39	482.5	67.1	463	4	US-09-472-087-4	Sequence 4, Appli
40	482.5	67.1	463	4	US-09-472-087-68	Sequence 68, Appl
41	480.5	66.8	456	4	US-09-495-880A-11	Sequence 11, Appl
42	478.5	66.6	135	3	US-08-619-491-4	Sequence 4, Appli
43	478.5	66.6	135	5	PCT-US95-07302-4	Sequence 4, Appli
44	477	66.3	239	2	US-08-553-497A-18	Sequence 18, Appl
45	475	66.1	123	3	US-09-344-587-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-08-579-378A-16

; Sequence 16, Application US/08579378A

; Patent No. 6210671

; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung

; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One MarketPlaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/579,378A
;      FILING DATE:  27-DEC-1995
;      CLASSIFICATION:  424
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/160,074
;      FILING DATE:  30-NOV-1993
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,946
;      FILING DATE:  01-DEC-1992
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95112895.8
;      FILING DATE:  17-AUG-1995
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95114696.8
;      FILING DATE:  19-SEP-1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebescheutz, Joe O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  11823-002220
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;      INFORMATION FOR SEQ ID NO:  16:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  135 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-579-378A-16

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Query Match          78.8%;  Score 566.5;  DB 3;  Length 135;
Best Local Similarity 81.2%;  Pred. No. 1.4e-52;
Matches 112;  Conservative 8;  Mismatches 15;  Indels 3;  Gaps 2;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| |||||||
Db      1 MNFGSSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      :||||| || || ||| |:|||||:|:| |||||:||||:| |
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Qy      121 YSGSSDYWGQGTTTVTVSS 138
      | | |||||:|
Db      118 YDGYFDYWGGQTTTLTVSS 135

```

RESULT 2

US-08-379-057-14

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; Sequence 14, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT:  Siadak, Anthony W.

```

```

; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their
Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,057
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0133-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 727-3670
; TELEFAX: (206) 727-3601
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-379-057-14

```

```

Query Match          78.3%; Score 563; DB 2; Length 138;
Best Local Similarity 79.1%; Pred. No. 3.3e-52;
Matches 110; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCTTSGFTFNNYAMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR-YD 119
      :||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     61 EKRLEWVASI-SSGDSTYYPDVVRGRFTISRDNARNILYLQMSSLRSEDTAMYYCARHYD 119

Qy    120 HYSGSSDYWGQGTTVTVSS 138
      : | : ||||| |||||
Db    120 YDSYAMDYWGQGTSTVTVSS 138

```

RESULT 3

US-08-653-402B-6

; Sequence 6, Application US/08653402B

; Patent No. 5969107

; GENERAL INFORMATION:

; APPLICANT: CARCELLER, Ana

; APPLICANT: ROSELL, Elisabet

; APPLICANT: GOMEZ, Alicia

; APPLICANT: ADEN, Jaume

; APPLICANT: PIULATS, Jaume

; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an

; TITLE OF INVENTION: immune response against epidermal growth factor receptor.

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

; STREET: 2200 Clarendon Boulevard, Suite 1400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/653,402B

; FILING DATE: 24-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95107967.2

; FILING DATE: 26-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lebovitz, Richard M.

; REGISTRATION NUMBER: 37,067

; REFERENCE/DOCKET NUMBER: MERCK 1781

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333

; TELEFAX: 703-243-6410

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 158 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-653-402B-6

Query Match 76.6%; Score 551; DB 2; Length 158;

Best Local Similarity 77.8%; Pred. No. 7.5e-51;

Matches 112; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

|:||||||||||| ||| |:||||||||||| | ||||||||||||||| |||||

Db 1 MDFGLSLIFLVLFKGVLCDEVKLVESGGGLVKLGSLKLSCAASGFTFSNYMSWVRQTP 60

```
Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY-- 118  
       :|||:|:| | || ||| | |||||||:||||||||||||||||||| |:  
Db      61 EKRLEFVAAINSNGGSTYYPDTVKGRFTISRDNKNTLYLQMSSLKSEDTALYYCARHRG 120  
  
Qy     119 ---DHYSG-SSDYWGQGTTVTVSS 138  
       | | : |||||:|||||  
Db     121 RDSSGYVGYAIDYWGQGSVTVSS 144
```

US-08-836-561-23

; Sequence 23, Application US/08836561

; GENERAL INFORMATION:

APPLICANT: FURUYA, Akiko

APPLICANT: NAKAMURA, Kazuyasu

; APPLICANT: IIDA, Akihiro

; APPLICANT: ANAZAWA, Hideharu

; APPLICANT: HANAI, No. 6018032uo

; APPLICANT: TAKATSU, Kiyoshi

; TITLE OF INVENTION: Antibody Against Human

; TITLE OF INVENTION: Receiv

```
; NUMBER OF SEQUENCES: 1
```

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 A

; CITY: New

; STATE: NY

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READ.

```
; MEDIUM TYPE: Diskette
```

```
;      COMPUTER:  IBM Compatible
```

```
; OPERATING SYSTEM: DOS
```

```
; SOFTWARE: FastSEQ Version 2.0
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; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/836,561

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 232384/95

FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

```
;      NAME:  Lawrence, III, Stanton T
```

REGISTRATION NUMBER: 25,736

REFERENCE/DOCKET NUMBER: 7005-115-999

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNIE

: INFORMATION FOR SEO ID NO: 23:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 140 amino acids

: TYPE: amino acid


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-434-122-23

```

```

Query Match          76.4%; Score 549; DB 4; Length 140;
Best Local Similarity 74.3%; Pred. No. 1e-50;
Matches 104; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| | : ||||| | : ||||| | ||||| | ||||| | ||||| | : || : || |
Db      1 MNFGLSLIFLALILKGVQCEVQLVESGGDLVKPGGSLKLSCAASGFTFSDYGMWIRQIS 60

Qy      61 DKRLEWVASIRSGGGRTYYSNDNVKGRFTISRENAKNTLYLQMSSEDTALYYCVRYDH 120
        ||| ||| : | |||  : : | : ||||| : || : ||||| | : || ||||| : || |
Db      61 DKRPEWVA AISGGSYIHFPDSLKGRFTVSRDNAKNTLYLEMSGLKSEDTAMYYCARRGF 120

Qy      121 YSG--SSDYWGQGTTVTVSS 138
        |   : ||||| | : |||||
Db      121 YGNYRAMDYWGQGTSTVTVSS 140

```

RESULT 6

PCT-US94-07659-2

; Sequence 2, Application PC/TUS9407659

; GENERAL INFORMATION:

```

; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

```

```

; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

```

```

Query Match          76.4%; Score 549; DB 5; Length 247;
Best Local Similarity 78.3%; Pred. No. 2.1e-50;
Matches 108; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| ||||:|||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGLRLIFLVLTCLKGVKCEVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDH 120
        :|||:|||| | |||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      61 EKRLDWVAYISSGGGGTYYPDTVKGRFTISRDNKNTLYLQMSLKS EDTAMYHCARGGV 120

Qy      121 YSGSSDYWGQGT TVTVSS 138
        | | || ||||| |||
Db      121 RRGYFDVWGAGT TVTVSS 138

```

```

RESULT 7
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000

```

```

; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

```

```

Query Match          75.9%; Score 545.5; DB 3; Length 135;
Best Local Similarity 79.0%; Pred. No. 2.3e-50;
Matches 109; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGSSLIFLVVLKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRERAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | ||||| | || ||| |:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 GKGLEWVASI-STGGSTYYPD SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR--D 117

Qy    121 YSGSSDYWGQGTTVTVSS 138
      | | ||||| |||||
Db    118 YDGYFDYWGGQTLTVTVSS 135

```

RESULT 8
 US-08-976-183A-33
 ; Sequence 33, Application US/08976183A
 ; Patent No. 6307026
 ; GENERAL INFORMATION:
 ; APPLICANT: King, David J.
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Owens, Raymond J.
 ; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
 ; TITLE OF INVENTION: ANTIGEN
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K. Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/976,183A
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/595,848
 ; FILING DATE: 02-FEB-1996
 ; APPLICATION NUMBER: PCT/GB93/02529
 ; FILING DATE: 10-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9225853.2
 ; FILING DATE: 10-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9315249.4
 ; FILING DATE: 22-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bernhard D. Saxe
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 40283/151/CARA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 136 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-976-183A-33

Query Match 75.2%; Score 541; DB 3; Length 136;
 Best Local Similarity 75.5%; Pred. No. 7.1e-50;
 Matches 108; Conservative 10; Mismatches 13; Indels 12; Gaps 2;

QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:||||| ||||| || |||||
 Db 1 MNFGLSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

QY 61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
 :|||||:| ||| ||| |:|||||:|:|||||:|||||
 Db 61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

QY 116 VRYDHYSGSSDYWGQGTTVTVSS 138
 | : ||||| ||||:
 Db 121 VPF-----AYWGQGTTLVTVSA 136

RESULT 9

US-08-976-183A-31

; Sequence 31, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

; APPLICANT: King, David J.

; APPLICANT: Adair, John R.

; APPLICANT: Owens, Raymond J.

; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K. Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/976,183A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,848

; FILING DATE: 02-FEB-1996

; APPLICATION NUMBER: PCT/GB93/02529

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9225853.2

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9315249.4

; FILING DATE: 22-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Bernhard D. Saxe

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 40283/151/CARA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELEX: 904136

```
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 136 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-976-183A-31
```

```
Query Match          75.1%; Score 540; DB 3; Length 136;
Best Local Similarity 74.8%; Pred. No. 9.1e-50;
Matches 107; Conservative 11; Mismatches 13; Indels 12; Gaps 2;
```

```
Qy      1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:||||:||||||||||||||||||| ||||| || | |||||
Db      1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
        :|||||:| ||| ||| |:|||||||:|:|||||||:|||||||
Db      61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy      116 VRYDHYSGSSDYWGQGTTVTVSS 138
        | :      ||||| ||||:
Db      121 VPF-----AYWGQGTTLVTVSA 136
```

RESULT 10

US-08-976-183A-32

```
; Sequence 32, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
;   APPLICANT: King, David J.
;   APPLICANT: Adair, John R.
;   APPLICANT: Owens, Raymond J.
;   TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
;   TITLE OF INVENTION: ANTIGEN
;   NUMBER OF SEQUENCES: 55
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: FOLEY & LARDNER
;     STREET: 3000 K. Street, N.W., Suite 500
;     CITY: Washington, D.C.
;     COUNTRY: USA
;     ZIP: 20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/976,183A
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/595,848
;     FILING DATE: 02-FEB-1996
;     APPLICATION NUMBER: PCT/GB93/02529
;     FILING DATE: 10-DEC-1993
;   PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-183A-32

```

```

Query Match          74.7%; Score 537; DB 3; Length 136;
Best Local Similarity 74.8%; Pred. No. 1.9e-49;
Matches 107; Conservative 10; Mismatches 14; Indels 12; Gaps 2;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      |||| |||||:|||||||||||||||||| ||||| || | |||||
Db      1 MNFGFSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
      :||| |||:| || | || |:|||||||:|:| ||||| ||||| |||
Db     61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy     116 VRYDHYSGSSDYWGQGTTVTVSS 138
      | :      ||||| ||||:
Db     121 VPF-----AYWGQGTTLVTVSA 136

```

RESULT 11

US-08-976-183A-34

; Sequence 34, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

; APPLICANT: King, David J.

; APPLICANT: Adair, John R.

; APPLICANT: Owens, Raymond J.

; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K. Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-183A-34

```

```

Query Match          74.5%; Score 536; DB 3; Length 136;
Best Local Similarity 74.1%; Pred. No. 2.4e-49;
Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| :|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGFSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRERAKNTLYLQMSSLKSEDTALYYC----- 115
      :|||||:| ||| ||| |:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy      116 VRYDHYSGSSDYWGQGTTVTVSS 138
      | : ||||| ||||:
Db      121 VPF-----AYWGQGTTLVTVSA 136

```

```

RESULT 12
US-08-253-877C-57
; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:

```

```

; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-253-877C-57

```

```

Query Match          74.4%; Score 535; DB 1; Length 136;
Best Local Similarity 74.1%; Pred. No. 3.1e-49;
Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
        :|||||:| ||| ||| |:|||||:|: :|||||:|||||:|||||:
Db     61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSRNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy    116 VRYDHYSGSSDYWGQGTTVTVSS 138
        | : ||||| ||||:
Db    121 VPF-----AYWGQGTTLVTVSA 136

```

RESULT 13

US-08-452-164A-57

; Sequence 57, Application US/08452164A

; Patent No. 5877296

; GENERAL INFORMATION:

; APPLICANT: Hamann, Philip R.

; APPLICANT: Hinman, Lois

; APPLICANT: Hollander, Irwin

; APPLICANT: Holcomb, Ryan

; APPLICANT: Hallett, William

; APPLICANT: Tsou, Hwei-Ru

; APPLICANT: Weiss, Martin J.

; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/452,164A

; FILING DATE: 26-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 32,368-04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2158

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 136 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-452-164A-57

Query Match 74.4%; Score 535; DB 2; Length 136;

Best Local Similarity 74.1%; Pred. No. 3.1e-49;

Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:||||:||||||||||||||||||| ||||| || || |||||

Db 1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYC----- 115
 :|||||:| ||| ||| |:|||||||::: :|||||||:|||||||

```

Db          61 EKRLEWVATISSGGSYTYYLDSVKGRFTISRDSPRNTLYLQMSSLRSEDALYYCAPTTV 120
Qy          116 VRYDHYSGSSDYWGQGTTVTVSS 138
              | :          ||||| ||||:
Db          121 VPF-----AYWGQGTTLVTVSA 136

```

RESULT 14

US-08-053-171-7

```

; Sequence 7, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Willaim M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-053-171-7

Query Match 74.4%; Score 535; DB 1; Length 138;
Best Local Similarity 75.4%; Pred. No. 3.1e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy	1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKGASLKLSCAASGFTFSNYGMSWVRQNS 60 : :
Db	1 MNLGLSLIFLVLVLKGVQCEVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTP 60
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120 : : :: : : : : :
Db	61 EKRLEWVAYISNGGGSSHYVDSVKGRFTISRDNKNTLYLOMSRLRSEDAMYHCARGMD 120

```
Qy      121 YSGSSDYWGQGTTVTVSS 138
          |      ||||| |||:
Db      121 YGAWFAYWGQGLTVTSA 138
```

```

RESULT 15
US-08-053-171-11
; Sequence 11, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Willaim M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-171-11

```

Query Match 74.4%; Score 535; DB 1; Length 138;
Best Local Similarity 75.4%; Pred. No. 3.1e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy	1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60 : :
Db	1 MNLGLSLIFLVLVLKGVQCEVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTP 60
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120 : : : : : : :
Db	61 EKRLEWVAYISNGGGSSHYVDSVKGRFTISRDNKNTLYLQMSRLRSEDAMYHCARGMD 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
| ||||| |||:
Db 121 YGAWFAYWGQGTTLVTVSA 138

Search completed: December 13, 2004, 19:19:41
Job time : 29.6222 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:04:43 ; Search time 24.5333 Seconds
 (without alignments)
 541.219 Million cell updates/sec

Title: US-10-010-942B-4
 Perfect score: 719
 Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	573	79.7	138	2	S09258	Ig heavy chain V r
2	569	79.1	152	2	B26471	Ig heavy chain pre.....
3	559.5	77.8	139	2	S38808	Ig heavy chain - m
4	544	75.7	142	2	C34903	Ig heavy chain pre
5	521.5	72.5	140	2	S70442	Ig heavy chain pre
6	517	71.9	140	2	S31686	Ig heavy chain V r
7	516	71.8	160	2	S05271	Ig heavy chain pre
8	514	71.5	134	2	S31699	Ig heavy chain V r
9	513	71.3	140	2	S31588	Ig heavy chain V r
10	512	71.2	117	1	HVMS84	Ig heavy chain pre
11	510	70.9	117	1	HVMS34	Ig heavy chain pre
12	508	70.7	136	2	S31615	hypothetical prote
13	504	70.1	140	2	S22657	Ig heavy chain pre

14	502.5	69.9	136	1	G1MS21	Ig heavy chain pre
15	502	69.8	138	2	S31666	Ig heavy chain V r
16	501	69.7	117	1	HVMS39	Ig heavy chain pre
17	495	68.8	135	2	S31598	Ig heavy chain V r
18	493	68.6	134	2	S31679	Ig heavy chain V r
19	492.5	68.5	141	2	S31669	Ig heavy chain V r
20	492	68.4	117	1	HVMSRF	Ig heavy chain pre
21	492	68.4	139	2	I37781	Ig variable region
22	490	68.2	122	2	E27888	Ig heavy chain V r
23	487.5	67.8	119	2	F27888	Ig heavy chain V r
24	485.5	67.5	136	2	S31587	Ig heavy chain V r
25	484.5	67.4	151	2	A60943	Ig heavy chain pre
26	484	67.3	117	1	HVMS57	Ig heavy chain pre
27	484	67.3	140	2	A30532	Ig heavy chain pre
28	483	67.2	120	2	S55536	Ig heavy chain V r
29	481.5	67.0	147	2	I37780	Ig variable region
30	480.5	66.8	118	2	PH0096	Ig heavy chain V r
31	480.5	66.8	121	2	S55540	Ig heavy chain V r
32	480.5	66.8	254	2	B31790	Ig heavy chain V r
33	479	66.6	120	2	S55538	Ig heavy chain V r
34	479	66.6	120	2	S55539	Ig heavy chain V r
35	477.5	66.4	121	2	H27888	Ig heavy chain V r
36	477.5	66.4	137	2	S31701	Ig heavy chain V r
37	477.5	66.4	139	2	S31674	Ig heavy chain V r
38	476.5	66.3	137	2	S78054	Ig heavy chain pre
39	476	66.2	120	2	S55537	Ig heavy chain V r
40	473.5	65.9	118	2	PH0097	Ig heavy chain V r
41	472	65.6	132	2	S31603	Ig heavy chain V r
42	471	65.5	130	2	PL0098	Ig heavy chain pre
43	469	65.2	118	2	S20641	Ig heavy chain V r
44	467.5	65.0	135	2	I37778	Ig variable region
45	467.5	65.0	145	2	S11239	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK16.

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 573; DB 2; Length 138;
 Best Local Similarity 80.4%; Pred. No. 5.8e-43;
 Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:||||| ||||| |||||:| |||||
Db      1 MNFGLSLIFLVILKGVQCEVILVESGGGLVKPGGSLKLSCAASGFTFSYTMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :|||||:| ||| ||| |:|||||:|||| |||||:||||| ||
Db      61 EKRLEWVATISSGGGNTYYPDVSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy      121 YSGSSDYWGQGTTVTVSS 138
        |      |||| |||:
Db      121 YEAWFASWGQGTTLVTVSA 138
  
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RESULT 2

B26471

Ig heavy chain precursor V region (MAK33) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C;Accession: B26471; S70410

R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987

A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a
 creatine-kinase-specific monoclonal antibody.

A;Reference number: A91572; MUID:87248058; PMID:3110009

A;Accession: B26471

A;Molecule type: mRNA

A;Residues: 1-152 <BUC>

A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406

R;Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 172, 1717-1727, 1990

A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5'
 boundary is near the promoter, and 3' boundary is about 1 kb from V(D)J gene.

A;Reference number: S70410; MUID:91079775; PMID:2258702

A;Accession: S70410

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-19 <LEB>

A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 569; DB 2; Length 152;
 Best Local Similarity 78.2%; Pred. No. 1.4e-42;
 Matches 111; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

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Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:||||| ||||| |||||:| |||||
  
```

```

Db          1 MNFGLSLIFLVLVLKGVQCEVQGVESGGGLVKPGGSLKLSCAASGFTFSFYMYWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
              :|||||||:| || ||| |:|||||||:|||| |||||:|||| |
Db          61 EKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKA 120
Qy          118 -YDHYSGSSDYWGQGTTVTVSS 138
              | :| : |||||:||||
Db          121 YYGNYGDAMDYWGQGTSVTVSS 142

```

RESULT 3

S38808

Ig heavy chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C;Accession: S38808

R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.

Immunogenetics 36, 15-21, 1992

A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2b antibody with rheumatoid factor activity.

A;Reference number: S38807; MUID:92267566; PMID:1587549

A;Accession: S38808

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <SEQ>

A;Cross-references: EMBL:X53400

A;Note: the authors translated the codon GAG for residue 117 as Lys

A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are not shown in this paper

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-116/Domain: immunoglobulin homology <IMM>

```

Query Match          77.8%;  Score 559.5;  DB 2;  Length 139;
Best Local Similarity 79.3%;  Pred. No. 8.7e-42;
Matches 111;  Conservative 8;  Mismatches 16;  Indels 5;  Gaps 2;

```

```

Qy          1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
              |||| |
Db          1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSYAMSWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
              :||||||| | || ||| |:|||||||:||:| |||||:||||:| |
Db          61 EKRLEWVASI-SRGGTTYYPDSVKGRFTISRDNARNNLYLQMSSLRSEDTAMYYCAREGI 119
Qy          121 YSG----SSDYWGQGTTVTV 136
              | | |||||:|
Db          120 YGYALYGM DYWGQGTSVTV 139

```

RESULT 4

C34903

Ig heavy chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C;Accession: C34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive anti-fluorescein monoclonal antibodies.

A;Reference number: A34903; MUID:90094387; PMID:2104617

A;Accession: C34903

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-142 <BED>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 544; DB 2; Length 142;
Best Local Similarity 76.1%; Pred. No. 2e-40;
Matches 108; Conservative 9; Mismatches 21; Indels 4; Gaps 2;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGFSLIFLVLVLKGVQCEVKWVESGGGLVSPGGSLKLSCAASGFTFSTYAMSWVRQTP 60

Qy     61 DKRLEWVASI--RSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY 118
      :||| ||| : ||||| |:||||| |:|:| |||||:||||:| |
Db     61 EKRLEWVASFGNKPTGGRTYYPDVKGRFTISRDNARNILYLQMSSLRSEDTAMYVCARG 120

Qy    119 DHYSGS--SDYWGQGTTVTVSS 138
      :| | ||||| |||:
Db    121 GYYYGGYWFAFWGQGTTLVTVSA 142
```

RESULT 5

S70442

Ig heavy chain precursor V region (mu) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: S70442

R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fetal B cells or a distinct B lineage?

A;Reference number: S70442; MUID:93024508; PMID:1383695

A;Accession: S70442

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: UNIPROT:Q8WUK1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 521.5; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 1.8e-38;
Matches 100; Conservative 18; Mismatches 19; Indels 3; Gaps 2;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | ||| :||| :|:||||:|:|||||:|:| | |:||||| ||||
Db      1 MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
```

```

Db      61 GKGLEWVAFIRYDGSNKYYADSVKGREFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR-DH 119
Qy      121 YSGSS--DYWGQGTTVTVSS 138
Db      120 IVGATYFDYWGOGLTVTVSS 139

```

RESULT 6

S31686

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text change 23-Jul-1999

C;Accession: S31686

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31686

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140. <CUI>

A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 517; DB 2; Length 140;

Best Local Similarity 70.7%; Pred. No. 4.4e-38;

Matches 99; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | : | | : | | | | | : : | | | | | : | | : | | | | | | | : | | | | |

Db 1 MEFGLSWLSLVAILKGVOCEVOLLESGGGLVOPGGSLRLSCAASGFTFSSYAMSWVROAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRTTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| | | | : | | | | : | | | : : | | | : | | : | | : |

Db 61 GKGLEWVSAISGSGGSTYYSDSVKGRFTISRDN SKNTLYLOMNSLRAEDTAVYYCAKCPF 120

Qy 121 YSGSS--DYWGQGTTVTVSS 138

Db 121 AGGSPSFDYWGOGLTVTVSS 140

RESULT 7

S05271

Ig heavy chain precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: S05271; S04602

R;Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A;Reference number: S05270

A;Accession: S05271

A;Molecule type: mRNA

A;Residues: 1-160 <KIS1>

A;Cross-references: UNIPROT:Q96BB9; EMBL:X14584
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04602
A;Molecule type: mRNA
A;Residues: 1-144 <KIS2>
A;Cross-references: EMBL:X14584
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 516; DB 2; Length 160;
Best Local Similarity 68.1%; Pred. No. 6.2e-38;
Matches 98; Conservative 18; Mismatches 22; Indels 6; Gaps 1;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | ||| :|| :|||||||:|:|||||||:| ||:||||||| | |||||
Db      1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
      | |||:| || |||:|:|||||||:|:|||||||:|:|:||||:| | :
Db     61 GKGLEWVSAISGGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAVV 120

Qy    118 ---YDHYSGSSDYWGQGT TTVTVSS 138
      :| | |||||||
Db    121 RGVISYYYYGMDVWGQGT TTVTVSS 144
```

RESULT 8

S31699

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31699

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31699

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <CUI>

A;Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 514; DB 2; Length 134;
Best Local Similarity 71.0%; Pred. No. 7.7e-38;
Matches 98; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        | | | | : | | | : | | | | | | : | : | | | | | | | | : | | | | |
Db      1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVHPGGSRLRLSCAASGFTFSSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        | | | | : | | | | | | : | | | | | | : | | | | | | : | | | | | | :
Db      61 GKGLEWVSAISGSGGSTYYSDSVKGRLTISRDNKNTLYLQMNSLRAEDTAVYYCARW-- 118

Qy      121 YSGSSDYWGQGTTVTVSS 138
        | | | | | | | | | |
Db      119 --RDL DYWGQGT LVT VSS 134

```

RESULT 9

S31588

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31588

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31588

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

```

Query Match          71.3%;  Score 513;  DB 2;  Length 140;
Best Local Similarity 69.3%;  Pred. No. 9.8e-38;
Matches 97;  Conservative 20;  Mismatches 21;  Indels 2;  Gaps 1;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        | | | | : | | | : | | | | | | : | : | | | | | | | | : | | | | |
Db      1 MEFGLSWLFLVAILRGVQCEVQLLESGGGLVQPGGSRLRLSCAASGFTFSSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        | | | | : | | | | | | : | | | | | | : | | | | | | : | | | | | | :
Db      61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDHD 120

Qy      121 YSG--SSDYWGQGTTVTVSS 138
        | | | | | | | | | |
Db      121 YSNYIYFDYWGQGT LVT VSS 140

```

RESULT 10

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C;Accession: JT0505

Query Match 70.9%; Score 510; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 1.5e-37;
Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| ||||:||||:||||||| ||||| ||||| ||:| |||||
Db      1 MNFGLRLIFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
        :||||||| | |||| ||| | ||||| ||||:||||||| ||||| ||||| |||||
Db      61 EKRLEWVAYISSGGGSTYYPDTVKGRFTISRDNKNTLYLQMSSLKSEDTAMYYCAR 117
```

RESULT 12

S31615

hypothetical protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C;Accession: S31615

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, April 1991

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for antidioxin monoclonal.

A;Reference number: S31615

A;Accession: S31615

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <REC>

A;Cross-references: EMBL:X58884; NID:g51824; PIDN:CAA41688.1; PID:g51825

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 508; DB 2; Length 136;
Best Local Similarity 70.3%; Pred. No. 2.6e-37;
Matches 97; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| |||||:| ||||| ||||| :||||:|||| || | | ||||
Db      1 MNFGLRLIFLVLTLKGVQCDVNLVESGGGLVKPGGTLKLSCSASGFAFSTYSMVWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :|||||||:| || ||| |:|:|||||||:|:|:| | |:| |||||:|||| |
Db      61 EKRLEWVATITGGGTYTYPPDSVRGRFTISRDNARDTLNLHMTNLKSEDTAMYYCLGYW 120

Qy      121 YSGSSDYWGQGTTVTVSS 138
        | |: ||||| | |:
Db      121 YDGT--YWGQGLVIVSA 136
```

RESULT 13

S22657

Ig heavy chain precursor V region (0-81VH) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 06-Feb-1998

C;Accession: S22657

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22657

A;Molecule type: mRNA

A;Residues: 1-140 <HIR>

A;Cross-references: EMBL:X59134

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 504; DB 2; Length 140;

Best Local Similarity 68.1%; Pred. No. 6e-37;

Matches 94; Conservative 21; Mismatches 19; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :|| :||:|||||:|||||||:| ||:|||||||:|: ||||

Db 1 MEFGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSSHWMTWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSLKSSEDALYYCVRYDH 120
||||||:| ||:|:|||||:||||:|||| ||::|||:||| |

Db 61 GKRLEWVANVKQDGSARYYADSVRGRFTISRDNAKNSLYLQMDSLRADDTAVYYCAR--- 117

Qy 121 YSGSSDYWGQGTTLTVTVSS 138
| ||||| ||||

Db 118 -STGIDYWGQGTTLTVTVSS 134

RESULT 14

G1MS21

Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C;Accession: E90809; A93184; A02066

R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: somatic mutation evident in a gamma2a variable region.

A;Reference number: A90809; MUID:81234548; PMID:6788376

A;Accession: E90809

A;Molecule type: mRNA

A;Residues: 1-136 <BOT>

A;Cross-references: UNIPROT:P01783; GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055

R;Adetugbo, K.; Milstein, C.; Secher, D.S.

Nature 265, 299-304, 1977

A;Title: Molecular analysis of spontaneous somatic mutants.

A;Reference number: A93184; MUID:77100368; PMID:401950

A;Contents: myeloma protein MOPC 21

A;Accession: A93184

A;Molecule type: protein

A;Residues: 17-74, 'D', 76-77, 'H', 79-88, 'ND', 91-114, 'H', 116-119, 'W', 121-136 <ADE>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
 F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>
 F;31-114/Domain: immunoglobulin homology <IMM>
 F;115-119/Region: D segment
 F;120-136/Region: J segment (JH4)
 F;38-112/Disulfide bonds: #status experimental

Query Match 69.9%; Score 502.5; DB 1; Length 136;
 Best Local Similarity 70.4%; Pred. No. 7.8e-37;
 Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

```

Qy      5 LSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      2 LNLVFLVLILKGVQCDVQLVESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPEKGL 61

Qy     65 EWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYS-G 123
          |||| | || :|:| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     62 EWWAYISSGSSTLHYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPYY 121

Qy    124 SSDYWGQGT TVTVSS 138
          : |||||::|::|::|
Db    122 AMDYWGQGT SVTVSS 136
  
```

RESULT 15

S31666

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31666

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
 submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
 from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31666

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-138 <CUI>

A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 502; DB 2; Length 138;
 Best Local Similarity 67.6%; Pred. No. 8.8e-37;
 Matches 96; Conservative 21; Mismatches 17; Indels 8; Gaps 2;

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          | |||| :|| :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
          | ||||::| || |||:|:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKART 120

Qy    118 -YDHYS GSSDYWGQGT TVTVSS 138
  
```

Db | :: | ||:| | ||| |
 121 GYWYF----DLWGRGTLVTVSS 138

Search completed: December 13, 2004, 19:18:39
Job time : 24.5333 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:17:53 ; Search time 99.1556 Seconds
(without alignments)
497.104 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	719	100.0	138	14	US-10-010-942B-4	Sequence 4, Appli
2	719	100.0	138	15	US-10-388-389-4	Sequence 4, Appli
3	719	100.0	138	16	US-10-703-713-4	Sequence 4, Appli
4	719	100.0	138	16	US-10-704-070-4	Sequence 4, Appli
5	652	90.7	138	14	US-10-010-942B-8	Sequence 8, Appli
6	652	90.7	138	15	US-10-388-389-8	Sequence 8, Appli
7	652	90.7	138	16	US-10-703-713-8	Sequence 8, Appli
8	652	90.7	138	16	US-10-704-070-8	Sequence 8, Appli
9	650	90.4	138	14	US-10-010-942B-12	Sequence 12, Appl
10	650	90.4	138	15	US-10-388-389-12	Sequence 12, Appl
11	650	90.4	138	16	US-10-703-713-12	Sequence 12, Appl
12	650	90.4	138	16	US-10-704-070-12	Sequence 12, Appl
13	609.5	84.8	133	13	US-10-006-773-9	Sequence 9, Appli
14	578.5	80.5	139	13	US-10-006-773-17	Sequence 17, Appl
15	578	80.4	462	14	US-10-281-479A-23	Sequence 23, Appl
16	578	80.4	462	14	US-10-286-132A-23	Sequence 23, Appl
17	578	80.4	464	14	US-10-275-180A-23	Sequence 23, Appl
18	569	79.1	144	9	US-09-881-823-12	Sequence 12, Appl
19	566	78.7	140	9	US-09-286-240-4	Sequence 4, Appli
20	559	77.7	140	13	US-10-006-773-4	Sequence 4, Appli
21	557.5	77.5	137	9	US-09-423-800-76	Sequence 76, Appl
22	557.5	77.5	137	14	US-10-337-981-76	Sequence 76, Appl
23	553	76.9	158	15	US-10-226-795-32	Sequence 32, Appl
24	549	76.4	140	14	US-10-283-349-23	Sequence 23, Appl
25	542	75.4	140	15	US-10-365-123-51	Sequence 51, Appl
26	537	74.7	159	14	US-10-291-265-333	Sequence 333, App
27	531.5	73.9	143	10	US-09-791-551-117	Sequence 117, App
28	528	73.4	143	15	US-10-469-304-17	Sequence 17, Appl
29	526.5	73.2	177	16	US-10-693-629-64	Sequence 64, Appl
30	522	72.6	313	14	US-10-291-265-427	Sequence 427, App
31	522	72.6	470	15	US-10-038-591-46	Sequence 46, Appl
32	522	72.6	470	17	US-10-775-444A-46	Sequence 46, Appl
33	520.5	72.4	469	14	US-10-292-088-54	Sequence 54, Appl
34	514.5	71.6	139	10	US-09-947-839-96	Sequence 96, Appl
35	514.5	71.6	139	17	US-10-478-056-33	Sequence 33, Appl
36	514	71.5	138	9	US-09-796-744-15	Sequence 15, Appl
37	514	71.5	138	14	US-10-231-452-62	Sequence 62, Appl
38	512	71.2	465	14	US-10-401-344-2	Sequence 2, Appli
39	510.5	71.0	137	9	US-09-423-800-77	Sequence 77, Appl
40	510.5	71.0	137	14	US-10-337-981-77	Sequence 77, Appl
41	510.5	71.0	473	15	US-10-038-591-50	Sequence 50, Appl
42	510.5	71.0	473	17	US-10-775-444A-50	Sequence 50, Appl
43	508.5	70.7	307	14	US-10-291-265-332	Sequence 332, App
44	508.5	70.7	363	14	US-10-291-265-335	Sequence 335, App
45	506	70.4	474	10	US-09-848-832-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-010-942B-4

; Sequence 4, Application US/10010942B

; Publication No. US20030165496A1

```
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4
```

```
Query Match          100.0%; Score 719; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.6e-60;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||
Db      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        |||
Db     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy     121 YSGSSDYWGQGTTVTTVSS 138
        |||
Db     121 YSGSSDYWGQGTTVTTVSS 138
```

RESULT 2

US-10-388-389-4

```
; Sequence 4, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-4

Query Match 100.0%; Score 719; DB 15; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.6e-60;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGT TVTVSS 138
||||||||||||||||
Db 121 YSGSSDYWGQGT TVTVSS 138

RESULT 3

US-10-703-713-4

; Sequence 4, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-4

Db 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTTVTVSS 138
 |||

Db 121 YSGSSDYWGQGTTTVTVSS 138

RESULT 5

US-10-010-942B-8

; Sequence 8, Application US/10010942B
 ; Publication No. US20030165496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basi, Guriq
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 ; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
 ; FILE REFERENCE: ELN-002
 ; CURRENT APPLICATION NUMBER: US/10/010,942B
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR APPLICATION NUMBER: US 60/251,892
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 138
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(19)
 US-10-010-942B-8

Query Match 90.7%; Score 652; DB 14; Length 138;
 Best Local Similarity 89.1%; Pred. No. 1.3e-53;
 Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||

Db 1 MNFGLSLIFLVLVLKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | |||

Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTTVTVSS 138
 |||

Db 121 YSGSSDYWGQGLTVTVSS 138

RESULT 6

US-10-388-389-8

; Sequence 8, Application US/10388389
 ; Publication No. US2004008777A1
 ; GENERAL INFORMATION:

```
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-8
```

```
Query Match          90.7%; Score 652; DB 15; Length 138;
Best Local Similarity 89.1%; Pred. No. 1.3e-53;
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:|:|||||:| ||:|||||
Db      1 MNFGLSLIFLVLVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        | |||||:|||||:|||||:|:|:|||||
Db     61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
        ||||| ||||
Db    121 YSGSSDYWGQGTTLVTVSS 138
```

RESULT 7

US-10-703-713-8

```
; Sequence 8, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
```

```
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-8
```

```
Query Match          90.7%; Score 652; DB 16; Length 138;
Best Local Similarity 89.1%; Pred. No. 1.3e-53;
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||:|||||:| ||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRDNKNTLYLQMSLKSSEDALYYCVRYDH 120
        | |||:|||||:| ||:|||||:| ||:|||||
Db     61 GKGLEWVASIRSGGGRITYSDNVKGRFTISRDNKNTLYLQMSLKSSEDALYYCVRYDH 120

Qy     121 YSGSSDYWGQGTTLTVSS 138
        |||
Db     121 YSGSSDYWGQGTTLTVSS 138
```

RESULT 8

US-10-704-070-8

```
; Sequence 8, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
```


Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||:|||||:| ||:|||||
 Db 1 MNFGLSLIFLVLVLKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | |||:|||||:| |:|||||
 Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
 |||
 Db 121 YSGSSDYWGQGTTLVTVSS 138

RESULT 10

US-10-388-389-12

; Sequence 12, Application US/10388389

; Publication No. US2004008777A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002CP

; CURRENT APPLICATION NUMBER: US/10/388,389

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 10/010,942

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized 3D6 light chain variable region

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(19)

US-10-388-389-12

Query Match 90.4%; Score 650; DB 15; Length 138;

Best Local Similarity 88.4%; Pred. No. 2.1e-53;

Matches 122; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||:|||||:| ||:|||||
 Db 1 MNFGLSLIFLVLVLKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | |||:|||||:| |:|||||
 Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138

Db 121 YSGSSDYWGQGLTVTVSS 138

RESULT 11

US-10-703-713-12

; Sequence 12, Application US/10703713

; Publication No. US20040171815A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002CP

; CURRENT APPLICATION NUMBER: US/10/703,713

; CURRENT FILING DATE: 2003-11-07

; PRIOR APPLICATION NUMBER: US/10/388,389

; PRIOR FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 10/010,942

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

```
; NUMBER OF SEQ ID NOS: 63
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEO ID NO 12

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

```
; OTHER INFORMATION: Humanized 3D6 light chain variable region
```

; FEATURE:

```
; NAME/KEY: SIGNAL
```

; LOCATION: (1) ... (19)

US-10-703-713-12

Query Match 90.4%; Score 650; DB 16; Length 138;
Best Local Similarity 88.4%; Pred. No. 2.1e-53;
Matches 122; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | | | | | | : : | | | | : | | : | | | |

Db 1 MNFGLSLIFLVVLKGVQCEVOLLES GGGLVOPGGSLRLSCAASGFTFSNYGMSWVROAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | | | | | | | | | | | | | | | | : : | | | | | | : : | | | | | |

Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCVRYDH 120

Qy 121 YSGSSDYWGQGTTVTVSS 138

Db 121 YSGSSDYWGQGLVTVSS 138

RESULT 12

US-10-704-070-12

; Sequence 12, Application US/10704070

; Publication No. US20040171816A1

```
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 light chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-704-070-12
```

```
Query Match          90.4%; Score 650; DB 16; Length 138;
Best Local Similarity 88.4%; Pred. No. 2.1e-53;
Matches 122; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:|:|||||:| ||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVQLLES GGGLVQPGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISR ENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          | |||||:|:|||||:|:|:|||||
Db     61 GKLEWVASIRSGGGRTYYSDNVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCVRYDH 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
          ||||| ||||
Db    121 YSGSSDYWGQGLTVTVSS 138
```

RESULT 13

US-10-006-773-9

```
; Sequence 9, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
```

; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-9

Query Match 84.8%; Score 609.5; DB 13; Length 133;
Best Local Similarity 87.0%; Pred. No. 1.3e-49;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||||||||||||||||:||||||||||||||||||||||||||| |
Db      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          ||||||||| ||| |:|:||||||||||||||||||||||||||| | |
Db     61 DKRLEWVASISSGGDSTFYADNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCARDL 120

Qy     121 YSGSSDYWGQGTTVTVSS 138
          :: |||||:||||
Db     121 FN-----WGQGTTLTVSS 133
```

RESULT 14

US-10-006-773-17

; Sequence 17, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-17

Query Match 80.5%; Score 578.5; DB 13; Length 139;
Best Local Similarity 82.7%; Pred. No. 1.1e-46;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          ||||||||||||||||||| |: |||||||||||||||:||||||||| |
Db      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFSNYGMSWVRQTS 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          ||||||||| :|| |:| |||||||||||||||||||||||||:| | |
```

```

Db          61 DKRLEWVASISTGGANTFYPDNVKGREFTISRENAKNTLYLQMSSLKSEDTALYFCARDSH 120
Qy          121 YSGS-SDYWGQGTTVTVSS 138
              |      ||||| ||||:
Db          121 SVGCWFATWGQGTLLTVSA 139

```

RESULT 15

US-10-281-479A-23

; Sequence 23, Application US/10281479A

; Publication No. US20030133932A1

; GENERAL INFORMATION:

; APPLICANT: The UAB Research Foundation

; APPLICANT: Zhou, Tong

; APPLICANT: Ichikawa, Kimihisa

; APPLICANT: Kimberly, Robert P.

; APPLICANT: Koopman, William J.

; APPLICANT: Oshumi, Jun

; APPLICANT: LoBuglio, Albert S.

; APPLICANT: Buchsbaum, Donald J.

; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS

; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND

OTHER THERAPEUTIC

: TITLE OF INVENTION: AGENTS

FILE REFERENCE: 21085.0029U6

; CURRENT APPLICATION NUMBER: US/10/281,479A

; CURRENT FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: 60/391,478

; PRIOR FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: 60/346,402

PRIOR FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: PCT/US01/14151

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,344

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 102

```
; SOFTWARE: PatentIn version 3.0
```

; SEQ ID NO 23

; LENGTH: 462

; TYPE: PRT

```
; ORGANISM: artificial sequence
```

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e

= Synthetic Construct

US-10-281-479A-23

Query Match 80.4%; Score 578; DB 14; Length 462;

Best Local Similarity 81.2%; Pred. No. 4.8e-46;

Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | : | | | | |

Db 1 MNFGLSLIFLVVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
:|||||:| ||| |:|||||:|||||:|||||:|||||

Db 61 EKRLWVATISSGGSYTYYPDSVKGRFTISRDNANTLYLOMSSLRSEDAMYYCARRGD 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
::|||||||:||||
Db 121 SMITTDYWGQGTTLTVSS 138

Search completed: December 13, 2004, 19:34:50
Job time : 100.156 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 18:50:06 ; Search time 131.356 Seconds
(without alignments)
604.479 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	576.5	80.2	487	2	Q99KA4	Q99ka4 mus musculu	
2	557	77.5	479	2	Q91WP5	Q91wp5 mus musculu	
3	547	76.1	486	2	Q91Z07	Q91z07 mus musculu	
4	529	73.6	485	2	Q6PDB8	Q6pdb8 mus musculu	
5	529	73.6	485	2	AAH58814	Aah58814 mus muscu	
6	516.5	71.8	473	2	Q91Z05	Q91z05 mus musculu	
7	512	71.2	117	1	HV54_MOUSE	P18525 mus musculu	
8	510	70.9	117	1	HV55_MOUSE	P18526 mus musculu	
9	505	70.2	480	2	Q91XE1	Q91xe1 mus musculu	
10	503	70.0	597	2	Q96BB9	Q96bb9 homo sapien	
11	502.5	69.9	136	1	HV16_MOUSE	P01783 mus musculu	
12	501	69.7	117	1	HV59_MOUSE	P18530 mus musculu	
13	499	69.4	478	2	Q6PI81	Q6pi81 homo sapien	
14	499	69.4	478	2	AAH41037	Aah41037 homo sapi	
15	495.5	68.9	606	2	Q6GMY2	Q6gmy2 homo sapien	

16	492	68.4	117	1	HV53_MOUSE	P18524 mus musculu
17	492	68.4	119	2	Q920E7	Q920e7 mus musculu
18	490	68.2	255	2	Q6KB05	Q6kb05 mus musculu
19	490	68.2	255	2	CAG34081	Cag34081 mus muscu
20	490	68.2	499	2	Q8N5K4	Q8n5k4 homo sapien
21	487	67.7	464	2	Q6MZU6	Q6mzu6 homo sapien
22	487	67.7	464	2	CAE45931	Cae45931 homo sapi
23	486.5	67.7	613	2	Q8WUK1	Q8wuk1 homo sapien
24	486	67.6	470	2	Q6PJA4	Q6pja4 homo sapien
25	486	67.6	470	2	AAH18747	Aah18747 homo sapi
26	484	67.3	117	1	HV58_MOUSE	P18529 mus musculu
27	483.5	67.2	573	2	Q8WU38	Q8wu38 homo sapien
28	477.5	66.4	471	2	AAH24289	Aah24289 homo sapi
29	475	66.1	472	2	Q6N089	Q6n089 homo sapien
30	475	66.1	472	2	CAE45781	Cae45781 homo sapi
31	473	65.8	493	2	Q6GMX2	Q6gmx2 homo sapien
32	471	65.5	493	2	Q8NCL6	Q8ncl6 homo sapien
33	468.5	65.2	475	2	Q6MZQ6	Q6mzq6 homo sapien
34	468.5	65.2	475	2	CAE45972	Cae45972 homo sapi
35	464	64.5	128	2	BAD00406	Bad00406 camelus d
36	464	64.5	464	2	BAC85395	Bac85395 homo sapi
37	463.5	64.5	465	2	Q6P6C4	Q6p6c4 homo sapien
38	463.5	64.5	465	2	AAH62335	Aah62335 homo sapi
39	463	64.4	117	1	HV3C_HUMAN	P01764 homo sapien
40	463	64.4	117	2	AAL35877	Aal35877 lama glam
41	462.5	64.3	479	2	AAH06402	Aah06402 homo sapi
42	461.5	64.2	494	2	Q96K68	Q96k68 homo sapien
43	460.5	64.0	473	2	Q6MZV7	Q6mzv7 homo sapien
44	460.5	64.0	473	2	CAE45920	Cae45920 homo sapi
45	460	64.0	497	2	BAC86210	Bac86210 homo sapi

ALIGNMENTS

RESULT 1

Q99KA4

ID Q99KA4 PRELIMINARY; PRT; 487 AA.

AC Q99KA4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE LOC380791 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II;
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC004786; AAH04786.1; -.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 80.2%; Score 576.5; DB 2; Length 487;
 Best Local Similarity 79.2%; Pred. No. 4.6e-49;
 Matches 114; Conservative 7; Mismatches 16; Indels 7; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||||||||||||||||||:||||||||||| |||||||||||||:| |||||
 Db 1 MNFGLSLIFLVLVLKGVQCEVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
 :|||||||:| || ||| |||||||||||:|||| ||||| |||||||:||| |
 Db 61 EKRLEWVATISDGGSYTYYPDNVKGRFTISRDNAKNNLYLQMSHLKSEDTAMYYCARDMG 120

 Qy 118 ---YDHYSGSSDYWGQGTITVTVSS 138
 | || |||||||:||||
 Db 121 GSPYGGYS-RFDYWGQGTITVTVSS 143

RESULT 2

Q91WP5

ID Q91WP5 PRELIMINARY; PRT; 479 AA.
 AC Q91WP5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Igh-VJ558 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC013656; AAH13656.1; -.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 77.5%; Score 557; DB 2; Length 479;
 Best Local Similarity 78.3%; Pred. No. 4e-47;
 Matches 108; Conservative 10; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||:||||| |||||:||||||| |||:||||| ||||| |||||:
 Db 1 MNFGLTLIFLVLTLLKGVQCEVQLVESGGGLVKPGGSLKVS CAASGLTFSNYAMSWVRQSP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

```

          :|||||:| | | | | :|||||:|:|:|:|:|:|:| | | |
Db        61 EKRLEWVAAINSNGGNTYYSDTMKGRFTISRDNASTLYLQMSSLRSEDATFYVCVR--- 117

Qy        121 YSGSSDYWGQGTTVTVSS 138
          | | | | | | | |
Db        118 -GGYFDVWGAGTAVTVSS 134

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RESULT 3

Q91Z07

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ID   Q91Z07          PRELIMINARY;          PRT;    486 AA.
AC   Q91Z07;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   LOC380791 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010324; AAH10324.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.

```


RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC058814; AAH58814.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.....
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 73.6%; Score 529; DB 2; Length 485;
 Best Local Similarity 71.4%; Pred. No. 2.6e-44;
 Matches 100; Conservative 17; Mismatches 21; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |: :|:||||:|||||:|:||||||| || | ||||| ||||| ||||
 Db 1 MDSRFNLVFLVLILKGVQCDVQLVESGGGLVPPGGSRLKSCAASGFTFSNYGMHWVRQAP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--Y 118
 :| ||||| | | | :|:| ||||| |||||:|||||:|:|:|:|:|:| | |
 Db 61 EGGLEWVAYISSSSGTIFYADTVKGRFTISRDNKNTLFLQMTSLRSEDTAMYYCARLYY 120

 Qy 119 DHYSGSSDYWGQGTTVTVSS 138
 :| |: |||||:|||||
 Db 121 SNYGGAMDYWGQGTSVTVSS 140

RESULT 5 AAH58814

ID AAH58814 PRELIMINARY; PRT; 485 AA.....
 AC AAH58814;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC010327; AAH10327.1; -.
 DR PIR; S68213; S68213.
 DR HSSP; P01783; 1IGC.
 DR MGD; MGI:2144967; AU044919.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 71.8%; Score 516.5; DB 2; Length 473;
 Best Local Similarity 72.5%; Pred. No. 4.5e-43;
 Matches 100; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Qy	1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKGASLKLSCAASGFTFSNYGMSSWVRQNS	60
	: : : : : : : : : : : : : : : :	
Db	1 MDSRLNLVFLVLILKGVQCEVQLVESGGGLVGPGGSRKLSAASGFTFSDDYGMHWVRQAP	60
Qy	61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVRYDH	120
	: : : : : : : : : :	
Db	61 EGGLEWVAYINSGSTTIYYADTVKGRFTISRDNAKNTLFLLMTSLRSEDAMYYCAR-EL	119
Qy	121 YSGSSDYWGQGTTVTVS	138
	: :	
Db	120 WLRRIDYWGOGTITVS	137

HV54 MOUSE

```

Qy      ... 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||
Db      1 MNFGLSLIFLVLVLKGVLCCEVKLVESGGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYCVR 117
          :|||
Db      61 EKRLEWVAYISNGGGSTYYPDTVKGRFTISRDNKNNLYLQMSLKSSEDAMYYCAR 117

```

RESULT 8

HV55 MOUSE

```

ID      HV55_MOUSE          STANDARD;          PRT;    117 AA.
AC      P18526;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V region 345 precursor.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/cJ;
RX      MEDLINE=89279149; PubMed=2499654;
RA      Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT      "Early onset of somatic mutation in immunoglobulin VH genes during the
RT      primary immune response.";
RL      J. Exp. Med. 169:2007-2019(1989).
CC      -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR      PIR; JT0502; HVMS34.
DR      HSSP; P01783; 1IGC.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL          1          19
FT      CHAIN           20         117      Ig heavy chain V region 345.
FT      DOMAIN          20         49      Framework-1.
FT      DOMAIN          50         54      Complementarity-determining-1.
FT      DOMAIN          55         68      Framework-2.
FT      DOMAIN          69         85      Complementarity-determining-2.
FT      DOMAIN          86        117      Framework-3.
FT      DISULFID         41        115      By similarity.
FT      NON_TER         117        117
SQ      SEQUENCE      117 AA;  12902 MW;  49380E4627ACA99A CRC64;

```

Query Match 70.9%; Score 510; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 4.1e-43;
Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| ||||| |::||:||||||| | ||||| ||:| |||||
 Db 1 MNFGLRLIFLVLTLLKGVKCEVOLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVROTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 :||||||| | |||| ||| | |||||||||:|||||||||||||||||||:|||| |
 Db 61 EKRLEWVAYISSGGGSTYYPDTVKGRFTISRDNKNTLYLQMSSLKSEDTAMYYCAR 117

RESULT 9

Q91XE1

ID Q91XE1 PRELIMINARY; PRT; 480 AA.
 AC Q91XE1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Igh-VJ558 protein (Fragment).
 GN Name=Igh-VJ558;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC010798; AAH10798.1; -.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1 1
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 70.2%; Score 505; DB 2; Length 480;
Best Local Similarity 72.3%; Pred. No. 6.5e-42;
Matches 99; Conservative 16; Mismatches 20; Indels 2; Gaps 1;

Qy 2 NFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSD 61
|||||||:|||||:||||||| ||:||||| ||| ||||| :
Db 1 NFGLSLIFLVLILKGVLCVKLVESGGGLVKPGGSLRLSCAASGFIFSNYSWVRQTPE 60

Qy 62 KRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHY 121
|||||||:| :| |:| |:| |||||:|:|:| |:| |||||:| | |:|
Db 61 KRLEWVATISNSGYATHYPDSMKGRFTISRDNQNTVLLQMTSLNSEDATVYYCTRGDYW 120

Qy 122 SGSSDYWGQGTTTVTVSS 138
| || |||||
Db 121 --YFDVWGAGTTTVTVSS 135

RESULT 10

Q96BB9

ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC015760; AAH15760.1; -.
 DR PIR; S05271; S05271.
 DR PIR; S24260; S24260.
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 4.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 70.0%; Score 503; DB 2; Length 597;
 Best Local Similarity 66.7%; Pred. No. 1.3e-41;
 Matches 96; Conservative 22; Mismatches 20; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | |||| :||| :|||||||:|:|||||||:| | :|||||||:|:| | :|||
 Db 1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVQPGGSLRLSCAASGF SFSSYAMNWVRQAP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDH 120
 | ||||:| | |||:|:|||||||:|:|:| |||||:|:|:| |||:| | :
 Db 61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDN RDTLYLQMN SLRAEDTAVYYCAKDPR 120

 Qy 121 -YSGS-----SDYWGQGT TVTVSS 138
 || | ||||| |||||
 Db 121 GYSASGNYTREDYWGQGT LVTVSS 144

RESULT 11

HV16_MOUSE

ID HV16_MOUSE STANDARD; PRT; 136 AA.
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";

```

RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; G1MS21.
DR PDB; 1IGC; X-ray; H=-.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW Signal.
FT NON_TER      1      1
FT SIGNAL       <1     16
FT CHAIN        17     136      Ig heavy chain V region MOPC 21.
FT DOMAIN      115     119      D segment.
FT DOMAIN      120     136      JH4 SEGMENT.
FT DISULFID     38     112
FT CONFLICT     75     78      HYAD -> DYAH (in Ref. 2).
FT CONFLICT     89     90      DN -> ND (in Ref. 2).
FT CONFLICT    115    115      W -> H (in Ref. 2).
FT CONFLICT    120    120      Y -> W (in Ref. 2).
FT STRAND       19     23
FT STRAND       26     28
FT TURN         30     31
FT STRAND       34     41
FT HELIX        45     47
FT STRAND       50     55
FT STRAND       61     67
FT TURN         69     70
FT STRAND       74     76
FT HELIX        78     80
FT STRAND       81     81
FT TURN         82     83
FT STRAND       84     89
FT TURN         90     93
FT STRAND       94     99
FT HELIX       104    106
FT STRAND      108    114
FT TURN       118    119
FT STRAND      125    126
FT STRAND      130    134
FT NON_TER     136    136

```

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 69.9%; Score 502.5; DB 1; Length 136;

Best Local Similarity 70.4%; Pred. No. 2.8e-42;

Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

```
Qy      5 LSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64
          |:|:||||:|||||:|:|||||||:| | | |||||:|:| | ||| :| |
Db      2 LNLVFLVLILKGVQCDVQLVESGGGLVQPGGSRKLSAASGFTFSSFGMHWRQAPEKGL 61

Qy     65 EWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDHYS-G 123
          |||| | || :|:| |||||:| | |||:|:|:|:|:|:| | | |: :|
Db     62 EWVAYISSGSSTLHYADTVKGRFTISRDNPKNTLFLQMTSLRSED TAMYCARWGNYPYY 121

Qy    124 SSDYWGGGTTVTVSS 138
          : |||||:|||||
Db    122 AMDYWGGGTSVTVSS 136
```

RESULT 12

HV59_MOUSE

ID HV59_MOUSE STANDARD; PRT; 117 AA.

AC P18530;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region 7-39 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/cJ;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR PIR; JT0507; HVMS39.

DR HSSP; P18529; 1I8K.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 Ig heavy chain V region 7-39.

FT DOMAIN 20 49 Framework-1.

FT DOMAIN 50 54 Complementarity-determining-1.

FT DOMAIN 55 68 Framework-2.

FT DOMAIN 69 85 Complementarity-determining-2.

FT DOMAIN 86 117 Framework-3.

FT DISULFID 41 115 By similarity.

FT NON_TER 117 117

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 69.4%; Score 499; DB 2; Length 478;
 Best Local Similarity 65.5%; Pred. No. 2.6e-41;
 Matches 97; Conservative 18; Mismatches 23; Indels 10; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | ||| :||| :|:|||||:|||||||:| ||:|||||||:| |||||
 Db 1 MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSYWMSWVRQAP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRNAKNTLYLQMSLKS EDTALYYCVR--- 117
 | |||||:|: | || |:|||||||:||||:|||||:|:|:||||:| |
 Db 61 GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAREFE 120
 Qy 118 -----YDHYSGSSDYWGQGT TVTVSS 138
 |:| | ||:|||||||
 Db 121 STMTTVNADY YFYMDVWGKGT TVTVSS 148

RESULT 14

AAH41037

ID AAH41037 PRELIMINARY; PRT; 478 AA.
 AC AAH41037;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC041037; AAH41037.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 69.4%; Score 499; DB 2; Length 478;
 Best Local Similarity 65.5%; Pred. No. 2.6e-41;
 Matches 97; Conservative 18; Mismatches 23; Indels 10; Gaps 1;

Qy 1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | ||| :||| :|:|||||:|||||||:| ||:|||||||:| |||||
 Db 1 MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSYWSWVRQAP 60

 Qy 61 DKRLEWVASIRSGGGRTYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
 | ||||:|: | || |:|||||||:||||:||||:|:|:||||:| |
 Db 61 GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFE 120

 Qy 118 -----YDHYSGSSDYWGQGTTVTVSS 138
 |:| | ||:|||||||
 Db 121 STMTTVNADYYYFYMDVWGKGTTVTVSS 148

RESULT 15

Q6GMY2

ID Q6GMY2 PRELIMINARY; PRT; 606 AA.
 AC Q6GMY2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC073758; AAH73758.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 4.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;

Query Match 68.9%; Score 495.5; DB 2; Length 606;
 Best Local Similarity 63.6%; Pred. No. 7.6e-41;
 Matches 98; Conservative 18; Mismatches 21; Indels 17; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | |||| :||| :||| ||||| :||| ||||| ||||| ||| :||| ||| :||
 Db 1 MEFGLSWVFLVAIIKGVQCQVLVESGGGLVKPGGSLRLSCAASGFTFSYYMSWIRQAP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRERAKNTLYLQMSSLKSEDTALYYCVR--- 117
 | |||| :|| | | | :||| ||||| :||| :||| :||| :||| :||| :|||
 Db 61 GKGLEWVSYISSSSSYTNYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARGGN 120
 Qy 118 -----YDHYSGSSDYWGQGTTVTVSS 138
 | :| | | ||||| |||||
 Db 121 GIAAAGRVVYAEDYIIYYG-MDVWGQGTTVTVSS 153

Search completed: December 13, 2004, 19:17:46
 Job time : 133.356 secs